EXHIBIT C: CLEAN VERSION OF PENDING CLAIMS
U.S. APPLICATION SERIAL NO. 09/616,849
(ATTORNEY DOCKET NO. 9301-044)

(as amended February 5, 2002)

1. (Amended) A method for evaluating binding properties of a probe to a target molecule, said method comprising comparing the amount of binding of molecules in a first sample to the probe with the amount of binding of molecules in a second sample to the probe, wherein:

(a) the first sample comprises a plurality of molecules of the target molecule; and

(b) the second sample comprises a plurality of different molecules,

wherein the first sample is at least 75% pure in said target molecule.

4. (Amended) The method of claim 1 wherein the first sample is at least 90% pure in said target molecule.

5. (Amended) The method of claim 4 wherein the first sample is at least 95% pure in said target molecule.

6. (Amended) The method of claim 5 wherein the first sample is at least 99% pure in said target molecule.

7. (Amended) The method of claim 1 wherein each of said plurality of different molecules in the second sample is different from the target molecule in the first sample.

8. (Amended) The method of claim 1 wherein a sensitivity of the probe is determined, wherein said sensitivity is the absolute amount of molecules of said target molecule that bind to said probe.

9. (Amended) The method of claim 8 wherein the sensitivity of the probe is determined from the amount of binding of molecules of the target molecule in the first sample to the probe.

10. (Amended) The method of claim 1 wherein a specificity of the probe is determined, wherein said specificity is the amount of molecules of said target molecule that bind to said probe relative to the amount of other molecules that bind to said probe under the same binding conditions.

11. (Amended) The method of claim 10 wherein the specificity of the probe is determined from a ratio of the amount of binding to the probe of the molecules of the target molecule in the first sample to the amount of binding to the probe of molecules of the different molecules in the second sample.

12. (Amended) The method of claim 1 wherein the molecules of the target molecule in the first sample are detectably labeled.

13. (Amended) The method of claim 1 wherein the molecules of the plurality of different molecules in the second sample are detectably labeled.

15. (Amended) The method of claim 1 wherein:

(a) the molecules of the target molecule in the first sample are detectably labeled with a first label; and

(b) the molecules of the plurality of different target molecules in the second sample are detectably labeled with a second label,

the first label being distinguishable from the second label.

16. The method of claim 15 wherein:
the first label is a first fluorescent molecule, and
the second label is a second fluorescent molecule.

17. The method of claim 1 wherein the probe is attached to the surface of a support.

18. The method of claim 1 wherein the probe is one of a plurality of probes.

19. (Amended) The method of claim 18 wherein the plurality of probes comprises probes in an array of probes,

said array having a support with at least one surface and different probes attached to said surface,

wherein each of said different probes is attached to the surface of the support in a different location.

20. (Amended) The method of claim 1 wherein the probe is a polynucleotide probe comprising a predetermined nucleotide sequence.

21. The method of claim 20 wherein the molecules of the same target molecule in the first sample are polynucleotide molecules.

22. (Amended) The method of claim 21 wherein the predetermined nucleotide sequence of the polynucleotide probe is complementary to at least a portion of the nucleotide sequence of the polynucleotide molecules in the first sample.

23. (Amended) The method of claim 21 wherein the molecules of the different target molecules in the second sample are polynucleotide molecules comprising polynucleotide sequences that are different from the nucleotide sequence of the polynucleotide molecules in the first sample.

24. The method of claim 20 wherein the polynucleotide probe is attached to a surface of a support.

25. (Amended) The method of claim 20 wherein the polynucleotide probe is one of a plurality of polynucleotide probes comprising different nucleotide sequences.

26. (Amended) The method of claim 25 wherein the plurality of polynucleotide probes comprises polynucleotide probes in an array of polynucleotide probes,

said array having a support with at least one surface and different polynucleotide

probes attached to said surface,

wherein each of said different polynucleotide probes attached to said surface is attached to the surface of the support in a different location.

27. (Amended) A method for evaluating binding properties of a polynucleotide probe comprising a predetermined nucleotide sequence to a target nucleotide sequence, said method comprising comparing the amount of hybridization of polynucleotides in a first sample to the polynucleotide probe with the amount of hybridization of polynucleotides in a second sample to the polynucleotide probe, wherein:

(a) the first sample comprises a plurality of polynucleotide molecules comprising said target nucleotide sequence; and

(b) the second sample comprises a plurality of different polynucleotide molecules wherein each different polynucleotide molecule comprises a sequence that is different from the nucleotide sequences of any other polynucleotide molecules in said plurality of different polynucleotide molecules,

wherein the first sample is at least 75% pure in polynucleotide molecules comprising said target nucleotide sequence.

28. (Amended) The method of claim 27 wherein the predetermined nucleotide sequence of the polynucleotide probe is complementary to at least a hybridizable portion of the target nucleotide sequence in the first sample.

29. (Amended) The method of claim 27 wherein the target polynucleotide sequence in the first sample is a nucleotide sequence of a gene or gene transcript of a cell or organism, or of an mRNA, cDNA or cRNA derived therefrom.

30. (Amended) The method of claim 27 wherein the plurality of different polynucleotide molecules in the second sample comprise nucleotide sequences of a plurality of genes or gene transcripts of a cell or organism.

33. (Amended) The method of claim 27 wherein the first sample is at least 90% pure

in said polynucleotide molecules comprising said target nucleotide sequence.

34. (Amended) The method of claim 33 wherein the first sample is at least 95% pure in said polynucleotide molecules comprising said target nucleotide sequence.

35. (Amended) The method of claim 34 wherein in the first sample is at least 99% pure in said polynucleotide molecules comprising said target nucleotide sequence.

36. (Twice Amended) The method of claim 27 wherein each different polynucleotide molecule in the second sample does not comprise the target nucleotide sequence.

37. (Amended) The method of claim 36 wherein:

(a) the target polynucleotide sequence in the first sample is a sequence of a gene or gene transcript of a cell or organism; and

(b) the second sample comprises a polynucleotide sample from a deletion mutant of the cell or organism,

wherein the deletion mutant of the cell or organism does not express the gene or gene transcript.

38. (Amended) The method of claim 27 wherein the plurality of different polynucleotide molecules in the second sample comprises:

(a) polynucleotide molecules comprising the target nucleotide sequence, and

(b) a plurality of different polynucleotide molecules, each comprising a different nucleotide sequence and each not comprising the target nucleotide sequence.

39. (Twice Amended) The method of claim 38 wherein:

(a) the target nucleotide sequence comprises a sequence of a gene or gene transcript of a cell or organism; and

(b) the second sample comprises a polynucleotide sample from a wild-type strain of the cell or organism,

wherein the wild-type strain of the cell or organism expresses the gene or gene transcript.

40. (Amended) The method of claim 27 wherein:

(a) the first sample further comprises polynucleotide molecules that do not comprise the target nucleotide sequence; and

(b) the second sample lacks said polynucleotide molecules comprising said target nucleotide sequence.

42. (Amended) The method of claim 41 wherein:

(a) the target nucleotide sequence is a sequence of a gene or gene transcript of a cell or organism;

(b) the first sample comprises a polynucleotide sample from a wild-type strain of the cell or organism which expresses the gene or gene transcript; and

(c) the second sample comprises a polynucleotide sample from a deletion mutant of the cell or organism which does not express the gene or gene transcript.

43. (Amended) The method of claim 27 wherein

(a) the first sample further comprises polynucleotide molecules that do not comprise the target nucleotide sequence; and

(b) the second sample comprises:

(i) polynucleotide molecules comprising the target nucleotide sequence, and

(ii) a plurality of different polynucleotide molecules, each different polynucleotide molecule comprising a different nucleotide sequence and not comprising the target nucleotide sequence,

wherein the amount of polynucleotide molecules in the first sample comprising the target nucleotide sequence differs by at least a factor of two from the amount of polynucleotide molecules in the second sample comprising the target nucleotide sequence.

44. (Amended) The method of claim 43 wherein the amount of polynucleotide molecules in the first sample comprising the target nucleotide sequence differs from the amount of polynucleotide molecules in the second sample comprising the target nucleotide sequence by at least a factor of four.

45. (Amended) The method of claim 43 wherein the amount of polynucleotide molecules in the first sample comprising the target nucleotide sequence differs from the amount of polynucleotide molecules in the second sample comprising the target nucleotide sequence by at least a factor of eight.

46. (Amended) The method of claim 43 wherein the amount of polynucleotide molecules in the first sample comprising the target nucleotide sequence differs from the amount of polynucleotide molecules in the second sample comprising the target nucleotide sequence by at least a factor of twenty.

47. (Amended) The method of claim 43 wherein the amount of polynucleotide molecules in the first sample comprising the target nucleotide sequence differs from the amount of polynucleotide molecules in the second sample comprising the target nucleotide sequence by at least a factor of 100.

48. The method of claim 43 wherein the amount of each different polynucleotide molecule in the plurality of different molecules of the first sample differs from the amount of the corresponding different polynucleotide molecule in the plurality of different polynucleotide molecules of the second sample by no more than a factor of 100.

49. The method of claim 43 wherein the amount of each different polynucleotide molecule in the plurality of different molecules of the first sample differs from the amount of the corresponding different polynucleotide molecule in the plurality of different polynucleotide molecules of the second sample by no more than a factor of 10.

50. The method of claim 43 wherein the amount of each different polynucleotide molecule in the plurality of different molecules of the first sample differs from the amount of the corresponding different polynucleotide molecule in the plurality of different polynucleotide molecules of the second sample by no more than 50%.

51. The method of claim 43 wherein the mean abundance of the different

polynucleotide molecules in the plurality of different polynucleotide molecules of the first sample differs from the mean abundance of the different polynucleotide molecules in the plurality of different polynucleotide molecules of the second sample by no more than a factor of two.

52. The method of claim 43 wherein the mean abundance of the different polynucleotide molecules in the plurality of different polynucleotide molecules of the first sample differs from the mean abundance of the different polynucleotide molecules in the plurality of different polynucleotide molecules of the second sample by no more than 50%.

53. The method of claim 43 wherein the mean abundance of the different polynucleotide molecules in the plurality of different polynucleotide molecules of the first sample differs from the mean abundance of the different polynucleotide molecules in the plurality of different polynucleotide molecules of the second sample by no more than 10%.

54. The method of claim 43 wherein the mean abundance of the different polynucleotide molecules in the plurality of different polynucleotide molecules of the first sample differs from the mean abundance of the different polynucleotide molecules in the plurality of different polynucleotide molecules of the second sample by no more than 1%.

55. (Amended) The method of claim 27 wherein a sensitivity of the polynucleotide probe is determined, wherein said sensitivity is the absolute amount of said polynucleotide molecules comprising said target nucleotide sequence that bind to said polynucleotide probe.

56. (Amended) The method of claim 55 wherein the sensitivity of the polynucleotide probe is determined from the amount of hybridization of said polynucleotide molecules in the first sample to the polynucleotide probe.

57. (Amended) The method of claim 27 wherein a specificity of the polynucleotide probe is determined, wherein said specificity is the amount of said polynucleotide molecules comprising said target nucleotide sequence that bind to said polynucleotide probe relative to

the amount of polynucleotide molecules not comprising said target nucleotide sequence that bind to the probe under the same binding conditions.

58. (Amended) The method of claim 57 wherein the specificity of the polynucleotide probe is determined from a ratio of the amount of hybridization of polynucleotide molecules in the first sample to the polynucleotide probe to the amount of hybridization of polynucleotide molecules in the second sample to the polynucleotide probe.

59. (Amended) The method of claim 27 wherein the polynucleotide molecules in the first sample are detectably labeled.

60. The method of claim 27 wherein the polynucleotide molecules in the second sample are detectably labeled.

61. The method of claim 59 or 60 wherein the polynucleotide molecules are labeled with a fluorescent molecule.

62. (Amended) The method of claim 27 wherein:

(a) the polynucleotide molecules in the first sample are labeled with a first label; and

(b) the polynucleotide molecules in the second sample are labeled with a second label,

the first label being distinguishable from the second label.

63. The method of claim 62 wherein:

the first label is a first fluorescent molecule, and

the second label is a second fluorescent molecule.

64. The method of claim 27 wherein the polynucleotide probe is attached to a surface of a support.

65. The method of claim 27 wherein the polynucleotide probe is one of a plurality of polynucleotide probes.

66. (Amended) The method of claim 65 wherein the plurality of polynucleotide probes comprises polynucleotide probes in an array of polynucleotide probes,

said array having a support with at least one surface and different polynucleotide probes attached to said surface,

wherein each of said different polynucleotide probes attached to said surface is attached to the surface of the support in a different location.

67. (Amended) A method for evaluating binding properties of a plurality of polynucleotide probes to a target nucleotide sequence wherein each polynucleotide probe in the plurality of polynucleotide probes comprises a predetermined nucleotide sequence,

said method comprising comparing the amount of hybridization of polynucleotides in a first sample to each polynucleotide probe in the plurality of polynucleotide probes with the amount of hybridization of polynucleotides in a second sample to each polynucleotide probe in the plurality of polynucleotide probes, wherein:

(a) the first sample comprises a plurality of polynucleotide molecules comprising said target nucleotide sequence; and

(b) the second sample comprises a plurality of different polynucleotide molecules wherein each different polynucleotide molecule comprises a nucleotide sequence that is different from nucleotide sequence of any other polynucleotide molecules in said plurality of different polynucleotide molecules,

wherein the first sample is at least 75% pure in polynucleotide molecules comprising said target nucleotide sequence.

68. (Amended) The method of claim 67 wherein the predetermined nucleotide sequence of each polynucleotide probe is complementary to at least a hybridizable portion of the target nucleotide sequence.

69. (Amended) The method of claim 67 wherein a sensitivity of each polynucleotide probe in the plurality of different polynucleotide probes is determined, wherein said sensitivity is the absolute amount of said polynucleotide molecules comprising said target nucleotide sequence that bind to said polynucleotide probe.

70. (Amended) The method of claim 69 wherein the sensitivity of each polynucleotide probe in the plurality of polynucleotide probes is determined from the amount of hybridization of the polynucleotide molecules comprising said target nucleotide sequence in the first sample to each polynucleotide probe in the plurality of polynucleotide probes.

71. (Amended) The method of claim 67 wherein a specificity of each polynucleotide probe in the plurality of different polynucleotide probes is determined, wherein said specificity is the amount of said polynucleotide molecules comprising said target nucleotide sequence that bind to said polynucleotide probe relative to the amount of polynucleotide molecules not comprising said target nucleotide sequence that bind to the probe under the same binding conditions.

72. (Amended) The method of claim 71 wherein the specificity of each polynucleotide probe in the plurality of polynucleotide probes is determined from a ratio of

(a) the amount of hybridization of the polynucleotide molecules comprising said target nucleotide sequence in the first sample to each polynucleotide probe to

(b) the amount of hybridization of the plurality of different polynucleotide molecules in the second sample to each polynucleotide probe.

73. The method of claim 67 wherein each polynucleotide probe in the plurality of polynucleotide probes is attached to a surface of a support.

74. (Amended) The method of claim 67 wherein the plurality of polynucleotide probes comprises polynucleotide probes in an array of probes,

said array having a support with at least one surface and different polynucleotide probes attached to said surface,

wherein each of said different polynucleotide probes attached to said surface in the plurality of probes is attached to the surface of the support in a different location.

75. (Amended) The method of claim 67 wherein the first sample comprises two or more different polynucleotide molecules

wherein none of the plurality of different polynucleotide molecules hybridizes or cross-hybridizes to a probe that also hybridizes or cross-hybridizes to another one of the plurality of different polynucleotide molecules.

81. The method of claim 1 further comprising, prior to said step of comparing, the steps of:

(i) contacting the probe with the first sample under conditions conducive to binding;

(ii) contacting the probe with the second sample under conditions conducive to binding;

(iii) detecting any binding that occurs between the probe and molecules in the first sample; and

(iv) detecting any binding that occurs between the probe and molecules in the second sample.

82. The method of claim 81, wherein said steps of contacting are performed concurrently.

83. The method of claim 82 wherein said steps of detecting are performed concurrently.

84. The method of claim 27 wherein:

polynucleotides in the first sample are labeled with a first label and polynucleotides in the second sample are labeled with a second label that is distinguishable from the first label;

and further comprising, prior to said step of comparing the steps of:

(i) concurrently contacting the polynucleotide probe with the first sample and the

second sample under conditions conducive to hybridization, and

(ii) detecting any binding that occurs between the polynucleotide probe and polynucleotides in the first sample and the second sample.

85. (Amended) The method of claim 84 wherein the second sample lacks polynucleotide molecules of said first sample.